

SEQUENCE LISTING

<110> Kennedy, Giulia
Kang, Sanmao
Reinhard, Christoph
Jefferson, Anne Bennett

<120> POLYNUCLEOTIDES RELATED TO COLON CANCER

<130> 2300-1663

<140> Unassigned

<141> 2001-06-14

<150> 60/211,835

<151> 2000-06-15

<160> 127

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 564

<212> DNA

<213> H. sapiens

<220>

<221> CDS

<222> (21)...(396)

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53

Met	Lys	Leu	Leu	Thr	His	Asn	Leu	Leu	Ser	Ser
1				5					10	

cat gtg cgg ggg gtg ggg tcc cgt ggc ttc ccc ctg cgc ctc cag gcc
101

His	Val	Arg	Gly	Val	Gly	Ser	Arg	Gly	Phe	Pro	Leu	Arg	Leu	Gln	Ala
			15					20					25		

acc gag gtc cgt atc tgc cct gtg gaa ttc aac ccc aac ttc gtg gcg
149

Thr	Glu	Val	Arg	Ile	Cys	Pro	Val	Glu	Phe	Asn	Pro	Asn	Phe	Val	Ala
		30					35					40			

cgt atg ata cct aaa gtg gag tgg tcg gcg ttc ctg gag gcg gcc gat
197

Arg	Met	Ile	Pro	Lys	Val	Glu	Trp	Ser	Ala	Phe	Leu	Glu	Ala	Ala	Asp
	45					50					55				

aac ttg cgt ctg atc cag gtg ccg aaa ggg ccg gtt gag gga tat gag
245

Asn	Leu	Arg	Leu	Ile	Gln	Val	Pro	Lys	Gly	Pro	Val	Glu	Gly	Tyr	Glu
60					65					70					75

gag aat gag gag ttt ctg agg acc atg cac cac ctg ctg ctg gag gtg
293

Glu Asn Glu Glu Phe Leu Arg Thr Met His His Leu Leu Leu Glu Val
80 85 90

gaa gtg ata gag ggc acc ctg cag tgc ccg gaa tct gga cgt atg ttc
341

Glu Val Ile Glu Gly Thr Leu Gln Cys Pro Glu Ser Gly Arg Met Phe
95 100 105

ccc atc agc cgc ggg atc ccc aac atg ctg ctg agt gaa gag gaa act
389

Pro Ile Ser Arg Gly Ile Pro Asn Met Leu Leu Ser Glu Glu Glu Thr
110 115 120

gag agt t gattgtgccca ggcgccagtt tttcttgta tgactgtgta tttttgtga
446

Glu Ser
125

tctataccct gtttccgaat tctgccgtgt gtatcccca cccttgaccc aatgacacca
506

aacacagtgt ttttgagctc ggtattatat attttttct cattaaaggt ttaaaacc
564

<210> 2

<211> 125

<212> PRT

<213> H. sapiens

<400> 2

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Gly	Ser	Arg	Gly	Phe	Pro	Leu	Arg	Leu	Gln	Ala	Thr	Glu	Val	Arg	Ile
		20						25					30		
Cys	Pro	Val	Glu	Phe	Asn	Pro	Asn	Phe	Val	Ala	Arg	Met	Ile	Pro	Lys
		35					40					45			
Val	Glu	Trp	Ser	Ala	Phe	Leu	Glu	Ala	Ala	Asp	Asn	Leu	Arg	Leu	Ile
	50					55					60				
Gln	Val	Pro	Lys	Gly	Pro	Val	Glu	Gly	Tyr	Glu	Glu	Asn	Glu	Glu	Phe
65					70					75				80	
Leu	Arg	Thr	Met	His	His	Leu	Leu	Leu	Glu	Val	Glu	Val	Ile	Glu	Gly
				85					90					95	
Thr	Leu	Gln	Cys	Pro	Glu	Ser	Gly	Arg	Met	Phe	Pro	Ile	Ser	Arg	Gly
			100					105					110		
Ile	Pro	Asn	Met	Leu	Leu	Ser	Glu	Glu	Thr	Glu	Ser				
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<210> 3

<211> 919

<212> DNA

<213> H. sapiens

<220>

<221> CDS

<222> (219) ... (693)

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 713
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 155

gaagtctgaa gaacgccttc atttcatgca aatctataag ctcttgcttt tggctttacc
 773
 atatgttggtg tctaattctcc ttctgagaag gacgaaaaac tttcttccaa gtgaagatcc
 833
 atttaagaac acatgtatattt acatgcctat aatatgctgg ttgtgtatgc tttgtctttt
 893
 aagttattaa aggaacgtct aaaaaa
 919

<210> 4
 <211> 158
 <212> PRT
 <213> H. sapiens

<400> 4
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 20 25 30
 Ser Pro Val His Leu Ala Ala Gly Ser Gly Leu Ala Cys Phe Leu Leu
 35 40 45
 Trp Gln Leu Gln Thr Gly Ala Asp Leu Asn Gln Gln Asp Val Leu Gly
 50 55 60
 Glu Ala Pro Leu His Lys Ala Ala Lys Val Gly Ser Leu Glu Cys Leu
 65 70 75 80
 Ser Leu Leu Val Ala Ser Asp Ala Gln Ile Asp Leu Cys Asn Lys Asn
 85 90 95
 Gly Gln Thr Ala Glu Asp Leu Ala Trp Ser Cys Gly Phe Pro Asp Cys
 100 105 110
 Ala Lys Phe Leu Thr Thr Ile Lys Cys Met Gln Thr Ile Lys Ala Ser
 115 120 125
 Glu His Pro Asp Arg Asn Asp Cys Val Ala Val Leu Arg Gln Lys Arg
 130 135 140
 Ser Leu Gly Ser Val Glu Asn Thr Ser Gly Lys Arg Lys Cys
 145 150 155

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 <213> H. sapiens

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 <222> (5)...(1760)

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 49
 Met Ala Pro Ser Thr Pro Leu Leu Thr Val Arg Gly Ser Glu Gly
 1 5 10 15
 ctg tac atg gtg aat gga cca cca cat ttt aca gaa agc aca gtg ttt
 97

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gga cct cat gca gct tta gct aat aaa agt ttc ttt aag gca gat aaa
673
Gly Pro His Ala Ala Leu Ala Asn Lys Ser Phe Phe Lys Ala Asp Lys
210 215 220

gtt aca atg ctg tgg aat aaa aaa gct act gct gtg ttg gta ata gct
721
Val Thr Met Leu Trp Asn Lys Lys Ala Thr Ala Val Leu Val Ile Ala
225 230 235

agc aca gat gtt gac aag aca gga gct tcc tac tat gga gaa caa act
769
Ser Thr Asp Val Asp Lys Thr Gly Ala Ser Tyr Tyr Gly Glu Gln Thr
240 245 250 255

cta cac tac att gca aca aat gga gaa agt gct gta gtg caa tta cca
817
Leu His Tyr Ile Ala Thr Asn Gly Glu Ser Ala Val Val Gln Leu Pro
260 265 270

aaa aat ggc ccc att tat gat gta gtt tgg aat tct agt tct act gag
865
Lys Asn Gly Pro Ile Tyr Asp Val Val Trp Asn Ser Ser Ser Thr Glu
275 280 285

ttt tgt gct gta tat ggt ttt atg cct gcc aaa gcg aca att ttc aac
913
Phe Cys Ala Val Tyr Gly Phe Met Pro Ala Lys Ala Thr Ile Phe Asn
290 295 300

ttg aaa tgt gat cct gta ttt gac ttt gga act ggt cct cgt aat gca
961
Leu Lys Cys Asp Pro Val Phe Asp Phe Gly Thr Gly Pro Arg Asn Ala
305 310 315

gcc tac tat agc cct cat gga cat ata tta gta tta gct gga ttt gga
1009
Ala Tyr Tyr Ser Pro His Gly His Ile Leu Val Leu Ala Gly Phe Gly
320 325 330 335

aat ctg agg gga caa atg gaa gtg tgg gat gtg aaa aac tac aaa ctt
1057
Asn Leu Arg Gly Gln Met Glu Val Trp Asp Val Lys Asn Tyr Lys Leu
340 345 350

att tct aaa ccg gtg gct tct gat tct aca tat ttt gct tgg tgc ccg
1105
Ile Ser Lys Pro Val Ala Ser Asp Ser Thr Tyr Phe Ala Trp Cys Pro
355 360 365

gat ggt gag cat att tta aca gct aca tgt gct ccc agg tta cgg gtt
1153
Asp Gly Glu His Ile Leu Thr Ala Thr Cys Ala Pro Arg Leu Arg Val
370 375 380

Cys Ala Val Tyr Gly Phe Met Pro Ala Lys Ala Thr Ile Phe Asn Leu
 290 295 300
 Lys Cys Asp Pro Val Phe Asp Phe Gly Thr Gly Pro Arg Asn Ala Ala
 305 310 315 320
 Tyr Tyr Ser Pro His Gly His Ile Leu Val Leu Ala Gly Phe Gly Asn
 325 330 335
 Leu Arg Gly Gln Met Glu Val Trp Asp Val Lys Asn Tyr Lys Leu Ile
 340 345 350
 Ser Lys Pro Val Ala Ser Asp Ser Thr Tyr Phe Ala Trp Cys Pro Asp
 355 360 365
 Gly Glu His Ile Leu Thr Ala Thr Cys Ala Pro Arg Leu Arg Val Asn
 370 375 380
 Asn Gly Tyr Lys Ile Trp His Tyr Thr Gly Ser Ile Leu His Lys Tyr
 385 390 395 400
 Asp Val Pro Ser Asn Ala Glu Leu Trp Gln Val Ser Trp Gln Pro Phe
 405 410 415
 Leu Asp Gly Ile Phe Pro Ala Lys Thr Ile Thr Tyr Gln Ala Val Pro
 420 425 430
 Ser Glu Val Pro Asn Glu Glu Pro Lys Val Ala Thr Ala Tyr Arg Pro
 435 440 445
 Pro Ala Leu Arg Asn Lys Pro Ile Thr Asn Ser Lys Leu His Glu Glu
 450 455 460
 Glu Pro Pro Gln Asn Met Lys Pro Gln Ser Gly Asn Asp Lys Pro Leu
 465 470 475 480
 Ser Lys Thr Ala Leu Lys Asn Gln Arg Lys His Glu Ala Lys Lys Ala
 485 490 495
 Ala Lys Gln Glu Ala Arg Ser Asp Lys Ser Pro Asp Leu Ala Pro Thr
 500 505 510
 Pro Ala Pro Gln Ser Thr Pro Arg Asn Thr Val Ser Gln Ser Ile Ser
 515 520 525
 Gly Asp Pro Glu Ile Asp Lys Lys Ile Lys Asn Leu Lys Lys Lys Leu
 530 535 540
 Lys Ala Ile Glu Gln Leu Lys Glu Gln Ala Ala Thr Gly Lys Gln Leu
 545 550 555 560
 Glu Lys Asn Gln Leu Glu Lys Ile Gln Lys Glu Thr Ala Leu Leu Gln
 565 570 575
 Glu Leu Glu Asp Leu Glu Leu Gly Ile
 580 585

<210> 7

<211> 1110

<212> DNA

<213> H. sapiens

<220>

<221> CDS

<222> (78)...(642)

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 110

Met Ala Asn Ser Gly Cys Lys Asp Val Thr Gly
 1 5 10

cca gat gag gag agt ttt ctg tac ttt gcc tac ggc agc aac ctg ctg
 158

tttttaacac ttgagaacag ggatctgggg gatctccacg tttgatccat tttcagcagt
 752
 gctctgaagg agtatcttac ttgggtgatt ccttgTTTTT agactataaa aagaaactgg
 812
 gataggagtt agacaattta aaaggggtgt atgagggcct gaaatatgtg acaaatgaat
 872
 gtgagtaccc cttctgtgaa cactgaaagc tattctcttg aattgatctt aagtgtctcc
 932
 ttgctctggg aaaagataga tttgtagctc acttgatgat ggtgctgggtg aattgctctg
 992
 ctctgtctga gatttttaaa aatcagctta atgagagtaa tctgcagaca attgataata
 1052
 acattttgaa aattggaaag atggtatact gtttttagag gaataaacgt atttgtgg
 1110

<210> 8
 <211> 188
 <212> PRT
 <213> H. sapiens

<400> 8
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 1 5 10 15
 Phe Leu Tyr Phe Ala Tyr Gly Ser Asn Leu Leu Thr Glu Arg Ile His
 20 25 30
 Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val Ala Arg Leu Gln Asp
 35 40 45
 Phe Lys Leu Asp Phe Gly Asn Ser Gln Gly Lys Thr Ser Gln Thr Trp
 50 55 60
 His Gly Gly Ile Ala Thr Ile Phe Gln Ser Pro Gly Asp Glu Val Trp
 65 70 75 80
 Gly Val Val Trp Lys Met Asn Lys Ser Asn Leu Asn Ser Leu Asp Glu
 85 90 95
 Gln Glu Gly Val Lys Ser Gly Met Tyr Val Val Ile Glu Val Lys Val
 100 105 110
 Ala Thr Gln Glu Gly Lys Glu Ile Thr Cys Arg Ser Tyr Leu Met Thr
 115 120 125
 Asn Tyr Glu Ser Ala Pro Pro Ser Pro Gln Tyr Lys Lys Ile Ile Cys
 130 135 140
 Met Gly Ala Lys Glu Asn Gly Leu Pro Leu Glu Tyr Gln Glu Lys Leu
 145 150 155 160
 Lys Ala Ile Glu Pro Asn Asp Tyr Thr Gly Lys Val Ser Glu Glu Ile
 165 170 175
 Glu Asp Ile Ile Lys Lys Gly Glu Thr Gln Thr Leu
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<210> 9
 <211> 965
 <212> DNA
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<220>
 <221> CDS
 <222> (79)...(232)

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gcagggggt agtgggat atg gcc aac tcg ggc tgc aag gac gtc acg ggt
111

Met Ala Asn Ser Gly Cys Lys Asp Val Thr Gly
1 5 10

cca gat gag gag agt ttt ctg tac ttt gcc tac ggc agc aac ctg ctg
159
Pro Asp Glu Glu Ser Phe Leu Tyr Phe Ala Tyr Gly Ser Asn Leu Leu
15 20 25

aca gag agg atc cac ctc cga aac ccc tcg gcg gcg ttc ttc tgt gtg
207
Thr Glu Arg Ile His Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val
30 35 40

gcc cgc ctg cag gca aga agg ggt t aaaagtggaa tgtatgttgt
252
Ala Arg Leu Gln Ala Arg Arg Gly
45 50

aatagaagtt aaagttgcaa ctcaagaagg aaaagaaata acctgtcgaa gttatctgat
312
gacaaattac gaaagtgtc ccccatcccc acagtataaa aagattatctt gcatgggtgc
372
aaaagaaaat ggtttgccgc tggagtatca agagaagtta aaagcaatag aaccaaata
432
ctatacagga aaggtctcag aagaaattga agacatcatc aaaaaggggg aaacacaaac
492
tctttagaac ataacagaat atatctaagg gtattctatg tgctaataata aaatattttt
552
aacacttgag aacagggatc tgggggatct ccacgtttga tccattttca gcagtgtctt
612
gaaggagtat cttacttggg tgattccttg ttttttagact ataaaaagaa actgggatag
672
gagttagaca atttaaaagg ggtgtatgag ggcctgaaat atgtgacaaa tgaatgtgag
732
tacccttct gtgaacactg aaagctattc tcttgaattg atcttaagtg tctccttgct
792
ctggtaaaag atagatttgt agctcacttg atgatgggtgc tgggtgaattg ctctgctctg
852
tctgagattt ttaaaaatca gcttaatgag agtaatctgc agacaattga taataacatt
912
ttgaaaattg gaaagatggt atactgtttt tagaggaata aacgtatttg tgg
965

<210> 10
<211> 51
<212> PRT
<213> H. sapiens

<400> 10
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1 5 10 15
Phe Leu Tyr Phe Ala Tyr Gly Ser Asn Leu Leu Thr Glu Arg Ile His
20 25 30

ccctgtcaca cccccaaccc cagggagggg ctgtcatagt cccagaggat aagcaatacc
 1260
 tattttctgac tgagtctccc agcccagacc cagggaccct nggcccgaag ctcagctcta
 1320
 agaaccgccc caacccctcc agctccaaat ctgagcctcc accacataga ctgaaactcc
 1380
 cctggcccca gccctctcct gcctggcctg gcctgggaca cctcctctct gccaggaggg
 1440
 aataaaagcc agcgccggga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
 1500
 aaaaaan
 1507

<210> 16
 <211> 716
 <212> DNA
 <213> H. sapiens

<220>
 <221> CDS
 <222> (16)...(538)

<400> 16
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 51

Met Ala Asp Val Leu Asp Leu His Glu Ala Gly Gly
 1 5 10

gaa gat ttc gcc atg gat gag gat ggg gac gag agc att cac aaa ctg
 99

Glu Asp Phe Ala Met Asp Glu Asp Gly Asp Glu Ser Ile His Lys Leu
 15 20 25

aaa gaa aaa gcg aag aaa cgg aag ggt cgc ggc ttt ggc tcc gaa gag
 147

Lys Glu Lys Ala Lys Lys Arg Lys Gly Arg Gly Phe Gly Ser Glu Glu
 30 35 40

ggg tcc cga gcg cgg atg cgt gag gat tat gac agc gtg gag cag gat
 195

Gly Ser Arg Ala Arg Met Arg Glu Asp Tyr Asp Ser Val Glu Gln Asp
 45 50 55 60

ggc gat gaa ccc gga cca caa cgc tct gtt gaa ggc tgg att ctc ttt
 243

Gly Asp Glu Pro Gly Pro Gln Arg Ser Val Glu Gly Trp Ile Leu Phe
 65 70 75

gta act gga gtc cat gag gaa gcc acc gaa gaa gac ata cac gac aaa
 291

Val Thr Gly Val His Glu Glu Ala Thr Glu Glu Asp Ile His Asp Lys
 80 85 90

ttc gca gaa tat ggg gaa att aaa aac att cat ctc aac ctc gac agg
 339

Phe Ala Glu Tyr Gly Glu Ile Lys Asn Ile His Leu Asn Leu Asp Arg
 95 100 105

00001501-00001501

cga aca gga tat ctg aag ggg tat act cta gtt gaa tat gaa aca tac
387

Arg Thr Gly Tyr Leu Lys Gly Tyr Thr Leu Val Glu Tyr Glu Thr Tyr
110 115 120

aag gaa gcc cag gct gct atg gag gga ctc aat ggc cag gat ttg atg
435

Lys Glu Ala Gln Ala Ala Met Glu Gly Leu Asn Gly Gln Asp Leu Met
125 130 135 140

gga cag ccc atc agc gtt gac tgg tgt ttt gtt cgg ggt cca cca aaa
483

Gly Gln Pro Ile Ser Val Asp Trp Cys Phe Val Arg Gly Pro Pro Lys
145 150 155

ggc aag agg aga ggt ggc cga aga cgc agc aga agt cca gac cgg aga
531

Gly Lys Arg Arg Gly Gly Arg Arg Arg Ser Arg Ser Pro Asp Arg Arg
160 165 170

cgt cgc t gacaggtcct ctgttgcca ggtgttctct tcaagattcc atttgaccat
588

Arg Arg

gcagccttgg acaaatagga ctgggggtgga acttgctgtg tttatattta atctcttacc
648

gtatatgcgt agtatttgag ttgcgaataa atgttccatt ttgttttcta caaaaaaaaa
708

aaaaaaaa

716

<210> 17

<211> 174

<212> PRT

<213> H. sapiens

<400> 17

Met Ala Asp Val Leu Asp Leu His Glu Ala Gly Gly Glu Asp Phe Ala
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Met Asp Glu Asp Gly Asp Glu Ser Ile His Lys Leu Lys Glu Lys Ala
20 25 30

Lys Lys Arg Lys Gly Arg Gly Phe Gly Ser Glu Glu Gly Ser Arg Ala
35 40 45

Arg Met Arg Glu Asp Tyr Asp Ser Val Glu Gln Asp Gly Asp Glu Pro
50 55 60

Gly Pro Gln Arg Ser Val Glu Gly Trp Ile Leu Phe Val Thr Gly Val
65 70 75 80

His Glu Glu Ala Thr Glu Glu Asp Ile His Asp Lys Phe Ala Glu Tyr
85 90 95

Gly Glu Ile Lys Asn Ile His Leu Asn Leu Asp Arg Arg Thr Gly Tyr
100 105 110

Leu Lys Gly Tyr Thr Leu Val Glu Tyr Glu Thr Tyr Lys Glu Ala Gln
115 120 125

Ala Ala Met Glu Gly Leu Asn Gly Gln Asp Leu Met Gly Gln Pro Ile
130 135 140

Ser Val Asp Trp Cys Phe Val Arg Gly Pro Pro Lys Gly Lys Arg Arg
 145 150 155 160
 Gly Gly Arg Arg Arg Ser Arg Ser Pro Asp Arg Arg Arg Arg
 165 170

<210> 18
 <211> 763
 <212> DNA
 <213> H. sapiens

<220>
 <221> CDS
 <222> (2)...(551)

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 49
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 1 5 10 15

gtg gag gtc ttc aga cag aat ctt ttc cag gag gct gag gaa ttc ctc
 97
 Val Glu Val Phe Arg Gln Asn Leu Phe Gln Glu Ala Glu Glu Phe Leu
 20 25 30

tac aga ttc ttg cca cag aaa atc ata tac ctg aat cag ctc ttg caa
 145
 Tyr Arg Phe Leu Pro Gln Lys Ile Ile Tyr Leu Asn Gln Leu Leu Gln
 35 40 45

gag gac tcc ctc aat gtg gct gac ttg act tcc ctc cgg gcc cca ctg
 193
 Glu Asp Ser Leu Asn Val Ala Asp Leu Thr Ser Leu Arg Ala Pro Leu
 50 55 60

gac atc ccc atc cca gac cct cca ccc aag gat gat gag atg gaa aca
 241
 Asp Ile Pro Ile Pro Asp Pro Pro Pro Lys Asp Asp Glu Met Glu Thr
 65 70 75 80

gat aag cag gag aag aaa gaa gtc cct aag tgt gga ttt ctc cct ggg
 289
 Asp Lys Gln Glu Lys Lys Glu Val Pro Lys Cys Gly Phe Leu Pro Gly
 85 90 95

aat gag aaa gtc ctg tcc ctg ctt gcc ctg gtt aag cca gaa gtc tgg
 337
 Asn Glu Lys Val Leu Ser Leu Leu Ala Leu Val Lys Pro Glu Val Trp
 100 105 110

act ctc aaa gag aaa tgc att ctg gtg att aca tgg atc caa cac ctg
 385
 Thr Leu Lys Glu Lys Cys Ile Leu Val Ile Thr Trp Ile Gln His Leu
 115 120 125

atc ccc aag att gaa gat gga aat gat ttt ggg gta gca atc cag gag
 433
 Ile Pro Lys Ile Glu Asp Gly Asn Asp Phe Gly Val Ala Ile Gln Glu

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130                               135                               140
aag gtg ctg gag agg gtg aat gcc gtc aag acc aaa gtg aag ctt tcc
481
Lys Val Leu Glu Arg Val Asn Ala Val Lys Thr Lys Val Lys Leu Ser
145                               150                               155                               160

aga caa cca ttt cca agt act tct cag aac gtg ggg atg ctg tgg cca
529
Arg Gln Pro Phe Pro Ser Thr Ser Gln Asn Val Gly Met Leu Trp Pro
165                               170                               175

agg cct cca agg aga ctc atg t aatggattac cgggccttgg tgcattgagcg
581
Arg Pro Pro Arg Arg Leu Met
180

agatgaggca gcctatgggg agctcagggc catggtgctg gacctgaggg ccttctatgc
641
tgagctttat catatcatca gcagcaacct ggagaaaatt gtcaacccaa aggggtgaaga
701
aaagccatct atgtactgaa cccgggacta gaaggaaaat aaatgatcta tatgttgtgt
761
gg
763

<210> 19
<211> 183
<212> PRT
<213> H. sapiens

<400> 19
Met Ala Lys Pro Cys Gly Val Arg Leu Ser Gly Glu Ala Arg Lys Gln
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Val Glu Val Phe Arg Gln Asn Leu Phe Gln Glu Ala Glu Glu Phe Leu
20 25 30
Tyr Arg Phe Leu Pro Gln Lys Ile Ile Tyr Leu Asn Gln Leu Leu Gln
35 40 45
Glu Asp Ser Leu Asn Val Ala Asp Leu Thr Ser Leu Arg Ala Pro Leu
50 55 60
Asp Ile Pro Ile Pro Asp Pro Pro Pro Lys Asp Asp Glu Met Glu Thr
65 70 75 80
Asp Lys Gln Glu Lys Lys Glu Val Pro Lys Cys Gly Phe Leu Pro Gly
85 90 95
Asn Glu Lys Val Leu Ser Leu Leu Ala Leu Val Lys Pro Glu Val Trp
100 105 110
Thr Leu Lys Glu Lys Cys Ile Leu Val Ile Thr Trp Ile Gln His Leu
115 120 125
Ile Pro Lys Ile Glu Asp Gly Asn Asp Phe Gly Val Ala Ile Gln Glu
130 135 140
Lys Val Leu Glu Arg Val Asn Ala Val Lys Thr Lys Val Lys Leu Ser
145 150 155 160
Arg Gln Pro Phe Pro Ser Thr Ser Gln Asn Val Gly Met Leu Trp Pro
165 170 175
Arg Pro Pro Arg Arg Leu Met
180

<210> 20

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<211> 790
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 <213> H. sapiens

<220>
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 <222> (240)...(585)

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 120
 catctacacc ttttgcacag ttcttgaaga caacgtcatc atccacactt cttttaactt
 180
 tgaagttggc ctgaggctgg gatgggccag tgagattaag gagagggttt ccgctcaga
 239
 atg ttt tcc ata cga atc ctc tct tct tca gct ttt tgt tct tgt tcc
 287
 Met Phe Ser Ile Arg Ile Leu Ser Ser Ser Ala Phe Cys Ser Cys Ser
 1 5 10 15
 ttc ctg gcc tgc tct tca gct ctt tct ttt tta att ttt tcc agt tct
 335
 Phe Leu Ala Cys Ser Ser Ala Leu Ser Phe Leu Ile Phe Ser Ser Ser
 20 25 30
 gca aga aga gct gca gta tca tca tca tca ctt tct tct tca aaa tct
 383
 Ala Arg Arg Ala Ala Val Ser Ser Ser Ser Leu Ser Ser Ser Lys Ser
 35 40 45
 tca tct tcc tca tct gtt aga ggg tca tct gca tca agg ttg gcg gca
 431
 Ser Ser Ser Ser Ser Val Arg Gly Ser Ser Ala Ser Arg Leu Ala Ala
 50 55 60
 gga atc tgg tct aac cgt ggc ttt ttt gac act gaa gag gag gtt gta
 479
 Gly Ile Trp Ser Asn Arg Gly Phe Phe Asp Thr Glu Glu Glu Val Val
 65 70 75 80
 tgt tct cgg gtt gga cga tcc cta ttt ttc tct ctt gca gca gct ctc
 527
 Cys Ser Arg Val Gly Arg Ser Leu Phe Phe Ser Leu Ala Ala Ala Leu
 85 90 95
 tct ctt tct tcc aac tct ctc ctg aag tca cgg tta cga acc tct tca
 575
 Ser Leu Ser Ser Asn Ser Leu Leu Lys Ser Arg Leu Arg Thr Ser Ser
 100 105 110
 ggg gca tcc t gagtagtctg tctgtatattt atctttgtat gagagggtag
 625
 Gly Ala Ser
 115

gtctctgctt gaatactgct ttgaaagttg gctcaaata ccttctcctt ttccccttcc
685
acctctggca ggttcaaagg ttggcctggc tgctgttgtc atcttttatg actggccgag
745
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790

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<213> H. sapiens

<400> 21
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1 5 10 15
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20 25 30
Ala Arg Arg Ala Ala Val Ser Ser Ser Leu Ser Ser Ser Lys Ser
35 40 45
Ser Ser Ser Ser Ser Val Arg Gly Ser Ser Ala Ser Arg Leu Ala Ala
50 55 60
Gly Ile Trp Ser Asn Arg Gly Phe Phe Asp Thr Glu Glu Glu Val Val
65 70 75 80
Cys Ser Arg Val Gly Arg Ser Leu Phe Phe Ser Leu Ala Ala Ala Leu
85 90 95
Ser Leu Ser Ser Asn Ser Leu Leu Lys Ser Arg Leu Arg Thr Ser Ser
100 105 110
Gly Ala Ser
115

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58

Met Lys
1

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106
Arg Pro Lys Leu Lys Lys Ala Ser Lys Arg Met Thr Cys His Lys Arg
5 10 15

tat aaa atc caa aaa aag gtt cga gaa cat cat cga aaa tta aga aag
154
Tyr Lys Ile Gln Lys Lys Val Arg Glu His His Arg Lys Leu Arg Lys
20 25 30

gag gct aaa aag cag ggt cac aag aag cct agg aaa gac cca gga gtt
202
Glu Ala Lys Lys Gln Gly His Lys Lys Pro Arg Lys Asp Pro Gly Val

35	40	45	50
cca aac agt gct ccc ttt aag gag gct ctt ctt agg gaa gct gag cta			
250			
Pro Asn Ser Ala	Pro Phe Lys Glu Ala	Leu Leu Arg Glu Ala	Glu Leu
	55	60	65
agg aaa cag agg ctt gaa gaa cta aaa cag cag cag aaa ctt gac agg			
298			
Arg Lys Gln Arg	Leu Glu Glu Leu Lys Gln Gln Gln Lys	Leu Asp Arg	
	70	75	80
cag aag gaa cta gaa aag aaa aga aaa ctt gaa act aat cct gat att			
346			
Gln Lys Glu Leu Glu Lys Lys Arg Lys Leu Glu Thr Asn Pro Asp Ile			
	85	90	95
aag cca tca aat gtg gaa cct atg gaa aag gag ttt ggg ctt tgc aaa			
394			
Lys Pro Ser Asn Val Glu Pro Met Glu Lys Glu Phe Gly Leu Cys Lys			
	100	105	110
act gag aac aaa gcc aag tcg ggc aaa cag aat tca aag aag ctg tac			
442			
Thr Glu Asn Lys Ala Lys Ser Gly Lys Gln Asn Ser Lys Lys Leu Tyr			
	115	120	125
tgc caa gaa ctt aaa aag gtg att gaa gcc tcc gat gtt gtc cta gag			
490			
Cys Gln Glu Leu Lys Lys Val Ile Glu Ala Ser Asp Val Val Leu Glu			
	135	140	145
gtg ttg gat gcc aga gat cct ctt ggt tgc aga tgt cct cag gta gaa			
538			
Val Leu Asp Ala Arg Asp Pro Leu Gly Cys Arg Cys Pro Gln Val Glu			
	150	155	160
gag gcc att gtc cag agt gga cag aaa aag ctg gta ctt ata tta aat			
586			
Glu Ala Ile Val Gln Ser Gly Gln Lys Lys Leu Val Leu Ile Leu Asn			
	165	170	175
aaa tca gat ctg gta cca aag gag aat ttg gag agc tgg cta aat tat			
634			
Lys Ser Asp Leu Val Pro Lys Glu Asn Leu Glu Ser Trp Leu Asn Tyr			
	180	185	190
ttg aag aaa gaa ttg cca aca gtg gtg ttc aga gcc tca aca aaa cca			
682			
Leu Lys Lys Glu Leu Pro Thr Val Val Phe Arg Ala Ser Thr Lys Pro			
	195	200	205
aag gat aaa ggg aag ata acc aag cgt gtg aag gca aag aag aat gct			
730			
Lys Asp Lys Gly Lys Ile Thr Lys Arg Val Lys Ala Lys Lys Asn Ala			
	215	220	225

gct cca ttc aga agt gaa gtc tgc ttt ggg aaa gag ggc ctt tgg aaa
778
Ala Pro Phe Arg Ser Glu Val Cys Phe Gly Lys Glu Gly Leu Trp Lys
230 235 240

ctt ctt gga ggt ttt cag gaa act tgc agc aaa gcc att cgg gtt gga
826
Leu Leu Gly Gly Phe Gln Glu Thr Cys Ser Lys Ala Ile Arg Val Gly
245 250 255

gta att ggt ttc cca aat gtg ggg aaa agc agc att atc aat agc tta
874
Val Ile Gly Phe Pro Asn Val Gly Lys Ser Ser Ile Ile Asn Ser Leu
260 265 270

aaa caa gaa cag atg tgt aat gtt ggt gta tcc atg ggg ctt aca agg
922
Lys Gln Glu Gln Met Cys Asn Val Gly Val Ser Met Gly Leu Thr Arg
275 280 285 290

agc atg caa gtt gtc ccc ttg gac aaa cag atc aca atc ata gat agt
970
Ser Met Gln Val Val Pro Leu Asp Lys Gln Ile Thr Ile Ile Asp Ser
295 300 305

ccg agc ttc atc gta tct cca ctt aat tcc tcc tct gcg ctt gct ctg
1018
Pro Ser Phe Ile Val Ser Pro Leu Asn Ser Ser Ser Ala Leu Ala Leu
310 315 320

cga agt cca gca agt att gaa gta gta aaa ccg atg gag gct gcc agt
1066
Arg Ser Pro Ala Ser Ile Glu Val Val Lys Pro Met Glu Ala Ala Ser
325 330 335

gcc atc ctt tcc cag gct gat gct cga cag gta gta ctg aaa tat act
1114
Ala Ile Leu Ser Gln Ala Asp Ala Arg Gln Val Val Leu Lys Tyr Thr
340 345 350

gtc cca ggc tac agg aat tct ctg gaa ttt ttt act atg ctt gct cag
1162
Val Pro Gly Tyr Arg Asn Ser Leu Glu Phe Phe Thr Met Leu Ala Gln
355 360 365 370

aga aga ggt atg cac caa aaa ggt gga atc cca aat gtt gaa ggt gct
1210
Arg Arg Gly Met His Gln Lys Gly Gly Ile Pro Asn Val Glu Gly Ala
375 380 385

gcc aaa ctg ctg tgg tct gag tgg aca ggt gcc tca tta gct tac tat
1258
Ala Lys Leu Leu Trp Ser Glu Trp Thr Gly Ala Ser Leu Ala Tyr Tyr
390 395 400

tgc cat ccc cct aca tct tgg act cct cct cca tat ttt aat gag agt
1306

Cys His Pro Pro Thr Ser Trp Thr Pro Pro Pro Tyr Phe Asn Glu Ser
 405 410 415
 att gtg gta gac atg aaa agc ggc ttc aat ctg gaa gaa ctg gaa aag
 1354
 Ile Val Val Asp Met Lys Ser Gly Phe Asn Leu Glu Glu Leu Glu Lys
 420 425 430
 aac aat gca cag agc ata aga gcc atc aag ggc cct cat ttg gcc aat
 1402
 Asn Asn Ala Gln Ser Ile Arg Ala Ile Lys Gly Pro His Leu Ala Asn
 435 440 445 450
 agc atc ctt ttc cag tct tcc ggt ctg aca aat gga ata ata gaa gaa
 1450
 Ser Ile Leu Phe Gln Ser Ser Gly Leu Thr Asn Gly Ile Ile Glu Glu
 455 460 465
 aag gac ata cat gaa gaa ttg cca aaa cgg aaa gaa agg aag cag gag
 1498
 Lys Asp Ile His Glu Glu Leu Pro Lys Arg Lys Glu Arg Lys Gln Glu
 470 475 480
 gag agg gag gat gac aaa gac agt gac cag gaa act gtt gat gaa gaa
 1546
 Glu Arg Glu Asp Asp Lys Asp Ser Asp Gln Glu Thr Val Asp Glu Glu
 485 490 495
 gtt gat gaa aac agc tca ggc atg ttt gct gca gaa gag aca ggg gag
 1594
 Val Asp Glu Asn Ser Ser Gly Met Phe Ala Ala Glu Glu Thr Gly Glu
 500 505 510
 gca ctg tct gag gag act aca gca ggt gaa cag tct aca agg tct ttt
 1642
 Ala Leu Ser Glu Glu Thr Thr Ala Gly Glu Gln Ser Thr Arg Ser Phe
 515 520 525 530
 atc ttg gat aaa atc att gaa gag gat gat gct tat gac ttc agt aca
 1690
 Ile Leu Asp Lys Ile Ile Glu Glu Asp Asp Ala Tyr Asp Phe Ser Thr
 535 540 545
 gat tat gtg t aacagaacaa tggtttttta tgattttttt ttttaacatt
 1740
 Asp Tyr Val
 ttaagcagac tgctaaactg ttctctgtat aagttatggt atgcatgagc tgtgtaaatt
 1800
 ttgtgaatat gtattatatt aaaaccaggc aacttggaat ccctaaattc tgtaaaaaga
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 1920
 aaaaaaaaaa aaaaaaaaaa
 1939

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 <211> 549
 <212> PRT
 <213> H. sapiens

<400> 23

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			20					25					30		
Arg	Lys	Glu	Ala	Lys	Lys	Gln	Gly	His	Lys	Lys	Pro	Arg	Lys	Asp	Pro
		35					40					45			
Gly	Val	Pro	Asn	Ser	Ala	Pro	Phe	Lys	Glu	Ala	Leu	Leu	Arg	Glu	Ala
	50					55					60				
Glu	Leu	Arg	Lys	Gln	Arg	Leu	Glu	Glu	Leu	Lys	Gln	Gln	Gln	Lys	Leu
65					70					75				80	
Asp	Arg	Gln	Lys	Glu	Leu	Glu	Lys	Lys	Arg	Lys	Leu	Glu	Thr	Asn	Pro
			85						90					95	
Asp	Ile	Lys	Pro	Ser	Asn	Val	Glu	Pro	Met	Glu	Lys	Glu	Phe	Gly	Leu
			100					105						110	
Cys	Lys	Thr	Glu	Asn	Lys	Ala	Lys	Ser	Gly	Lys	Gln	Asn	Ser	Lys	Lys
		115					120					125			
Leu	Tyr	Cys	Gln	Glu	Leu	Lys	Lys	Val	Ile	Glu	Ala	Ser	Asp	Val	Val
	130					135					140				
Leu	Glu	Val	Leu	Asp	Ala	Arg	Asp	Pro	Leu	Gly	Cys	Arg	Cys	Pro	Gln
145					150					155					160
Val	Glu	Glu	Ala	Ile	Val	Gln	Ser	Gly	Gln	Lys	Lys	Leu	Val	Leu	Ile
				165					170					175	
Leu	Asn	Lys	Ser	Asp	Leu	Val	Pro	Lys	Glu	Asn	Leu	Glu	Ser	Trp	Leu
		180						185					190		
Asn	Tyr	Leu	Lys	Lys	Glu	Leu	Pro	Thr	Val	Val	Phe	Arg	Ala	Ser	Thr
		195					200					205			
Lys	Pro	Lys	Asp	Lys	Gly	Lys	Ile	Thr	Lys	Arg	Val	Lys	Ala	Lys	Lys
	210					215					220				
Asn	Ala	Ala	Pro	Phe	Arg	Ser	Glu	Val	Cys	Phe	Gly	Lys	Glu	Gly	Leu
225					230					235					240
Trp	Lys	Leu	Leu	Gly	Gly	Phe	Gln	Glu	Thr	Cys	Ser	Lys	Ala	Ile	Arg
				245					250					255	
Val	Gly	Val	Ile	Gly	Phe	Pro	Asn	Val	Gly	Lys	Ser	Ser	Ile	Ile	Asn
			260					265					270		
Ser	Leu	Lys	Gln	Glu	Gln	Met	Cys	Asn	Val	Gly	Val	Ser	Met	Gly	Leu
		275					280					285			
Thr	Arg	Ser	Met	Gln	Val	Val	Pro	Leu	Asp	Lys	Gln	Ile	Thr	Ile	Ile
	290					295					300				
Asp	Ser	Pro	Ser	Phe	Ile	Val	Ser	Pro	Leu	Asn	Ser	Ser	Ser	Ala	Leu
305					310					315					320
Ala	Leu	Arg	Ser	Pro	Ala	Ser	Ile	Glu	Val	Val	Lys	Pro	Met	Glu	Ala
				325					330					335	
Ala	Ser	Ala	Ile	Leu	Ser	Gln	Ala	Asp	Ala	Arg	Gln	Val	Val	Leu	Lys
			340					345					350		
Tyr	Thr	Val	Pro	Gly	Tyr	Arg	Asn	Ser	Leu	Glu	Phe	Phe	Thr	Met	Leu
		355					360					365			
Ala	Gln	Arg	Arg	Gly	Met	His	Gln	Lys	Gly	Gly	Ile	Pro	Asn	Val	Glu
	370					375					380				
Gly	Ala	Ala	Lys	Leu	Leu	Trp	Ser	Glu	Trp	Thr	Gly	Ala	Ser	Leu	Ala
385					390					395					400
Tyr	Tyr	Cys	His	Pro	Pro	Thr	Ser	Trp	Thr	Pro	Pro	Pro	Tyr	Phe	Asn

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      405      410      415
Glu Ser Ile Val Val Asp Met Lys Ser Gly Phe Asn Leu Glu Glu Leu
      420      425      430
Glu Lys Asn Asn Ala Gln Ser Ile Arg Ala Ile Lys Gly Pro His Leu
      435      440      445
Ala Asn Ser Ile Leu Phe Gln Ser Ser Gly Leu Thr Asn Gly Ile Ile
      450      455      460
Glu Glu Lys Asp Ile His Glu Glu Leu Pro Lys Arg Lys Glu Arg Lys
465      470      475      480
Gln Glu Glu Arg Glu Asp Asp Lys Asp Ser Asp Gln Glu Thr Val Asp
      485      490      495
Glu Glu Val Asp Glu Asn Ser Ser Gly Met Phe Ala Ala Glu Glu Thr
      500      505      510
Gly Glu Ala Leu Ser Glu Glu Thr Thr Ala Gly Glu Gln Ser Thr Arg
      515      520      525
Ser Phe Ile Leu Asp Lys Ile Ile Glu Glu Asp Asp Ala Tyr Asp Phe
      530      535      540
Ser Thr Asp Tyr Val
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<211> 503
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<213> H. sapiens

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ggg aag gtg att ggg aca aaa atg caa aag act gct aaa gtg aga gtg
99
Gly Lys Val Ile Gly Thr Lys Met Gln Lys Thr Ala Lys Val Arg Val
15      20      25      30

acc agg ctt gtt ctg gat ccc tat tta tta aag tat ttt aat aag cgg
147
Thr Arg Leu Val Leu Asp Pro Tyr Leu Leu Lys Tyr Phe Asn Lys Arg
      35      40      45

aaa acc tac ttt gct cac gat gcc ctt cag cag tgc aca gtt ggg gat
195
Lys Thr Tyr Phe Ala His Asp Ala Leu Gln Gln Cys Thr Val Gly Asp
      50      55      60

att gtg ctt ctc aga gct tta cct gtt cca cga gca aag cat gtg aaa
243
Ile Val Leu Leu Arg Ala Leu Pro Val Pro Arg Ala Lys His Val Lys
      65      70      75

cat gaa ctg gct gag atc gtt ttc aaa gtt gga aaa gtc ata gat cca
291
His Glu Leu Ala Glu Ile Val Phe Lys Val Gly Lys Val Ile Asp Pro

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      80              85              90
gtg aca gga aag ccc tgt gct gga act acc tac ctg gag agt ccg ttg
339
Val Thr Gly Lys Pro Cys Ala Gly Thr Thr Tyr Leu Glu Ser Pro Leu
 95              100              105              110

agt tcg gaa acc acc cag cta agc aaa aat ctg gaa gaa ctc aat atc
387
Ser Ser Glu Thr Thr Gln Leu Ser Lys Asn Leu Glu Glu Leu Asn Ile
      115              120              125

tct tca gca cag t gaagcgggag tggaagaagg atctgaaggg aaaaactgac
440
Ser Ser Ala Gln
      130

atgtttatgt tatggaaaaa gaaatttttc taagtttcat cacaaaaaaaa aaaaaaaaaa
500
aaa
503

<210> 25
<211> 130
<212> PRT
<213> H. sapiens

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      20              25              30
Leu Val Leu Asp Pro Tyr Leu Leu Lys Tyr Phe Asn Lys Arg Lys Thr
      35              40              45
Tyr Phe Ala His Asp Ala Leu Gln Gln Cys Thr Val Gly Asp Ile Val
      50              55              60
Leu Leu Arg Ala Leu Pro Val Pro Arg Ala Lys His Val Lys His Glu
      65              70              75              80
Leu Ala Glu Ile Val Phe Lys Val Gly Lys Val Ile Asp Pro Val Thr
      85              90              95
Gly Lys Pro Cys Ala Gly Thr Thr Tyr Leu Glu Ser Pro Leu Ser Ser
      100              105              110
Glu Thr Thr Gln Leu Ser Lys Asn Leu Glu Glu Leu Asn Ile Ser Ser
      115              120              125
Ala Gln
      130
<210> 26
<211> 651
<212> DNA
<213> H. sapiens

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120

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tcctaaagag caagcctaac tcaagccatt ggcacacagg cattagacag aaagctggaa
180
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240
ttttatccat ggatgacttg cttgggtaag gacatgaaga cagttcctgt catacctttt
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360
ctcagaattc atgattgaag aaatgcaggc agacctgtta tcctaaacta gggtttttaa
420
tgaccacaac aagcaagcat gcagcttact gcttgaaagg gtcttgctc acccaagcta
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<210> 27
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120
gaagttgaaa tgggtggagtc caacttgctt ggaccagctt aatgggttctg ctctggtaa
180
cgtttttatc catggatgac ttgcttgggt atggagagtc ggcttgacta cactgtgtgg
240
agcaagtttt aaagaagcaa aggactcaga attcatgatt gaagaaatgc aggcagacct
300
gttatcctaa actagggttt tta atg acc aca aca agc aag cat gca gct tac
353

Met Thr Thr Thr Ser Lys His Ala Ala Tyr
1 5 10

tgc ttg aaa ggg tct tgc ctc acc caa gct aga gtg cag tgg cct ttg
401
Cys Leu Lys Gly Ser Cys Leu Thr Gln Ala Arg Val Gln Trp Pro Leu
15 20 25

aag ctt act aca gcc tca aac ttc tgg gct caa gtg atc ctc agc ctc
449
Lys Leu Thr Thr Ala Ser Asn Phe Trp Ala Gln Val Ile Leu Ser Leu
30 35 40

cca gtg gtc ttt gta gac tgc ctg atg gag tct cat ggc aca aga aga
497
Pro Val Val Phe Val Asp Cys Leu Met Glu Ser His Gly Thr Arg Arg

45

50

55

tta aaa cag tgt ctc caa ttt t aataaatttt tgcaatccaa aaaaaaaaaa
549

Leu Lys Gln Cys Leu Gln Phe
60 65

aaaaaaaaaa
559

<210> 28
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<213> H. sapiens

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Asn Phe Trp Ala Gln Val Ile Leu Ser Leu Pro Val Val Phe Val Asp
35 40 45
Cys Leu Met Glu Ser His Gly Thr Arg Arg Leu Lys Gln Cys Leu Gln
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Phe
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gtaacgtttt tatccatgga tgacttgctt gggatatggag agtcggcttg actacactgt
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tcaaacttct gggctcaagt gatcctcagc ctcccagtgg tctttgtaga ctgcctgatg
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caaaaaaaaaa aaaaaaaaaa aaa
623

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<220>
<223> Primer

<400> 30
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<210> 31
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<400> 31
tcaagggttg gggatacaca cg
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<210> 32
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<212> DNA
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<220>
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<400> 32
cttgcttgct ttcttctctg gc
22

<210> 33
<211> 24
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<220>
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<400> 33
agtctggaaa tccacatgac caag
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<210> 34
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<210> 37
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<400> 37
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<210> 38
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<220>
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<400> 38
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<210> 39
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<212> DNA
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<400> 39
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<210> 40
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<220>
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<400> 40
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<220>
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<400> 43
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<210> 44
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<220>
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